

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/531,415  
Source: PCT  
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## RAW SEQUENCE LISTING

DATE: 02/22/2006

PATENT APPLICATION: US/10/531,415

TIME: 08:25:12

Input Set : A:\20057-002 SEQ.txt

Output Set: N:\CRF4\02222006\J531415.raw

5 <110> APPLICANT: BERDEL, Wolfgang  
 6 MULLER-TIDOW, Carsten  
 7 SERVE, Hubert  
 8 STEFFEN, Bjorn  
 10 <120> TITLE OF INVENTION: Delocalization Molecules and Use Thereof  
 12 <130> FILE REFERENCE: 20057.002  
 14 <140> CURRENT APPLICATION NUMBER: US 10/531,415  
 C--> 15 <141> **CURRENT FILING DATE: 2005-04-15**  
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/011525  
 18 <151> PRIOR FILING DATE: 2003-10-17  
 20 <150> PRIOR APPLICATION NUMBER: DE 102 48 751.0  
 21 <151> PRIOR FILING DATE: 2002-10-18  
 23 <160> NUMBER OF SEQ ID NOS: 13  
 25 <170> SOFTWARE: PatentIn version 3.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 497  
 29 <212> TYPE: PRT  
 30 <213> ORGANISM: artificial sequence  
 32 <220> FEATURE:  
 33 <223> OTHER INFORMATION: Amino acid sequence of GFP-M&M  
 35 <400> SEQUENCE: 1  
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 38 1 5 10 15  
 41 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 42 20 25 30  
 45 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 46 35 40 45  
 49 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 50 55 60  
 53 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 54 65 70 75 80  
 57 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 58 85 90 95  
 61 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 62 100 105 110  
 65 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 66 115 120 125  
 69 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 70 130 135 140  
 73 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 74 145 150 155 160  
 77 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 78 165 170 175

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82          180          185          190
85 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
86          195          200          205
89 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
90          210          215          220
93 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly
94 225          230          235          240
97 Thr Val Ile Ala Asn Tyr Leu Pro Asn Arg Thr Asp Val Gln Cys Gln
98          245          250          255
101 His Arg Trp Gln Lys Val Leu Asn Pro Glu Leu Ile Lys Gly Pro Trp
102          260          265          270
105 Thr Lys Glu Glu Asp Gln Arg Val Ile Glu Leu Val Gln Lys Tyr Gly
106          275          280          285
109 Pro Lys Arg Trp Ser Val Ile Ala Lys His Leu Lys Gly Arg Ile Gly
110          290          295          300
113 Lys Gln Cys Arg Glu Arg Trp His Asn His Leu Asn Pro Glu Val Lys
114 305          310          315          320
117 Lys Thr Ser Trp Thr Glu Glu Glu Asp Arg Ile Ile Tyr Gln Ala His
118          325          330          335
121 Lys Arg Leu Gly Asn Arg Trp Ala Glu Ile Ala Lys Leu Leu Pro Gly
122          340          345          350
125 Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn Ser Thr Met Arg Arg
126          355          360          365
129 Lys Val Glu Gln Glu Gly Tyr Gly Ser Ala Thr Ser His Thr Met Ser
130          370          375          380
133 Thr Ala Glu Val Leu Leu Asn Met Glu Ser Pro Ser Asp Ile Leu Asp
134 385          390          395          400
137 Glu Lys Gln Ile Phe Ser Thr Ser Glu Met Leu Pro Asp Ser Asp Pro
138          405          410          415
139 Ala Pro Ala Val Thr Leu Pro Asn Tyr Leu Phe Pro Ala Ser Glu Pro
140          420          425          430
143 Asp Ala Leu Asn Arg Ala Gly Asp Thr Ser Asp Gln Glu Gly His Ser
144          435          440          445
147 Leu Glu Glu Lys Ala Ser Arg Glu Glu Ser Ala Lys Lys Thr Gly Lys
148          450          455          460
151 Ser Lys Lys Arg Ile Arg Lys Thr Lys Gly Asn Arg Ser Thr Ser Pro
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155 Val Thr Asp Pro Ser Ile Pro Ile Arg Lys Lys Ser Lys Asp Gly Lys
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159 Gly
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165 <212> TYPE: DNA
166 <213> ORGANISM: artificial sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: Nucleotide sequence of GFP-M&M
171 <400> SEQUENCE: 2
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60

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175 ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgagggcgga tgccacctac 120
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179 ctcgtagacca cctgacctg cggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240
181 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc 300
183 ttcaaggacg acggcaacta caagaccgcg gccgaggtga agttcgaggg cgacaccctg 360
185 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctgggggac 420
187 aagctggagt acaactacaa cagccacaac gtctatatca tggccgacaa gcagaagaac 480
189 ggcatacagg tgaacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
191 gaccactacc agcagaacac ccccatcggc gacggccccg tgetgctgcc cgacaaccac 600
193 tacctgagca cccagtccgc cctgagcaaa gacccaacg agaagcgcg tccatgggtc 660
195 ctgctggagt tcgtgaccgc cgccgggatc actctcgga tggacgagct gtacaagggt 720
197 accgtcattg ccaattatct gcccaaccgg acagatgtgc agtgccaaca ccggtggcag 780
199 aaagtgtcta accctgaact catcaaagg cctggacca aagaagaaga tcagagagtc 840
201 atagagcttg tccagaataa tggccgaag cgttggtctg ttattgcaa gcacttaaaa 900
203 gggagaattg gaaagcagtg tcgggagagg tggcacaacc atttgaatcc agaagttaag 960
205 aaaacctcct ggacagaaga ggaggacaga atcatttacc aggcacacaa gcgtctgggg 1020
207 aacagatggg cagagatcgc aaagctgctg cccggacgga ctgataatgc tatcaagaac 1080
209 cactggaatt ccaccatgcg tcgcaagggt gaacaggaag gctacggatc cgccacctcg 1140
211 cacaccatgt caaccgcgga agtcttactc aatatggagt ctcccagcga tatcctggat 1200
213 gagaagcaga tcttcagtac ctccgaaatg cttccagact cggaccctgc accagctgtc 1260
215 actctgccc actacctgtt tcctgcctct gagcccgatg cctgaacag ggcgggtgac 1320
217 actagtgacc aggaggggca ttctctggag gagaaggcct ccagagagga aagtgccaa 1380
219 aagactggga aatcaaagaa gagaatccgg aagaccaagg gcaaccgaag tacctcacct 1440
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227 <213> ORGANISM: artificial sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Oligonucleotide primer MEF-BamHI for
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238 <211> LENGTH: 30
239 <212> TYPE: DNA
240 <213> ORGANISM: artificial sequence
242 <220> FEATURE:
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255 <220> FEATURE:
256 <223> OTHER INFORMATION: Oligonucleotide primer myb-KpnI for
258 <400> SEQUENCE: 5
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273 cagagaggat ccgtagcctt cctgttccac 30
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278 <212> TYPE: DNA
279 <213> ORGANISM: artificial sequence
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312 <400> SEQUENCE: 9
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336 <223> OTHER INFORMATION: cDNA EGFP
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344 ttcaccgggg tggtgcccat cctggtcgag ctggacggcg acgtaaacgg ccacaagttc 180

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350	gtgcagtgtc	tcagccgcta	ccccgaccac	atgaagcagc	acgacttctt	caagtccgcc	360
352	atgcccgaag	gctacgtcca	ggagcgcacc	atcttcttca	aggacgacgg	caactacaag	420
354	accgcgcgcg	aggtgaagtt	cgagggcgac	accctggtga	accgcatcga	gctgaagggc	480
356	atcgacttca	aggaggacgg	caacatcctg	gggcacaagc	tggagtacaa	ctacaacagc	540
358	cacaacgtct	atatcatggc	cgacaagcag	aagaacggca	tcaaggtgaa	cttcaagatc	600
360	cgccacaaca	tcgaggacgg	cagcgtgcag	ctcgccgacc	actaccagca	gaacaccccc	660
362	atcggcgacg	gccccgtgct	gctgcccagc	aaccactacc	tgagcaccga	gtccgcccctg	720
364	agcaaagacc	ccaacgagaa	gcgcgatcac	atggctctgc	tggagtctgt	gaccgcgcgc	780
366	gggatcactc	tcggcatgga	cgagctgtac	aagtaaagcg	gccgcgactc	tagatcataa	840
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370	tgaacctgaa	acataaaatg	aatgcaattg	ttgtgtttaa	cttgtttatt	gcagcttata	960
372	atggttacaa	ataaagcaat	agcatcacaa	atttcacaaa	taaagcattt	ttttcactgc	1020
374	attctagttg	tggtttgtcc	aaactcatca	atgtatctta	aggcgtaa	tgtaagcggt	1080
376	aatattttgt	taaaattcgc	gttaaatatt	tgtaaatca	gctcattttt	taaccaatag	1140
378	gccgaaatcg	gcaaaatccc	ttataaatca	aaagaataga	ccgagatagg	gttgagtgtt	1200
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